

Listing of Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application.

1. (Original) A nucleic acid hybridization probe which will hybridize to a nonrepetitive portion of target nucleic acid, said probe comprising a labeled, single copy human nucleic acid sequence of known sequence, said probe having a length of at least about 2000 nucleotides, said probe being free of the repeat sequences identified as SEQ ID Nos. 1-428 and 447-479 and subsequences thereof, said subsequences containing at least 17 nucleotides, at least a portion of the human nucleic acid sequence being derived either from an intron or an intergenic region wherein an intergenic region begins either upstream of the transcription initiation site or downstream of the polyadenylation site, and said probe being complementary to a non-repetitive portion of the target.

2. (Original) The probe of claim 1, said human nucleic acid sequence being human genomic DNA.

3. (Original) The probe of claim 2, said human genomic DNA being derived directly from PCR amplification of human genomic DNA.

4. (Original) The probe of claim 1, said human nucleic acid sequence being single stranded.

5. (Original) A modified human DNA sequence isolated from its natural environment which will hybridize to a portion of target human DNA, said sequence comprising a single copy

human DNA sequence of known sequence having a length of at least about 2000 nucleotides and being free of the repeat sequences identified as SEQ ID Nos. 1-428, 447-479, and subsequences thereof, said subsequences containing at least 17 nucleotides, at least a portion of the human nucleic acid sequence being derived from an intron or an intergenic region wherein an intergenic region begins either upstream of the transcription initiation site or downstream of the polyadenylation site, and said probe being complementary to a non-repetitive portion of the target.

6. (Original) The human DNA sequence of claim 5, said human DNA sequence being single stranded.

7. (Original) A hybridization method including the steps of contacting a target nucleic acid sequence with a probe in accordance with claim 1 under conditions permitting the probe to hybridize to at least a portion of said target nucleic acid sequence.

8. (Original) A hybridization method including the steps of annealing a target human DNA sequence to a single copy human DNA sequence in accordance with claim 5 under conditions permitting the single copy human DNA sequence to hybridize to at least a portion of said target human DNA sequence.

9. (Original) A method of developing a hybridization probe for a target nucleic acid sequence, said method comprising the steps of:

determining the sequence of at least one single copy sequence in said target nucleic acid sequence computationally, said determining step comprising the steps of ascertaining the nucleotide-by-nucleotide sequence of said target nucleic acid sequence, comparing said ascertained sequences with the sequences of known repeat sequences in said target nucleic acid sequence, and identifying said single copy sequence from said comparison, said known repeat sequences appearing at least 10 times in the genome and having at least about 50 nucleotides; and

developing a hybridization probe comprising a sequence complementary to a non-repetitive portion of the target which hybridizes to at least a part of said identified single copy sequence.

10. (Original) A method of identifying a single copy sequence interval from a target nucleic acid sequence computationally, said method comprising the steps of ascertaining the nucleotide-by-nucleotide sequence of said target nucleic acid sequence, comparing said ascertained sequences with the sequences of known repeat sequences in said target nucleic acid sequence, said known repeat sequences appearing at least 10 times in the genome and having at least about 50 nucleotides, and identifying said single copy sequence from said comparison.

11. (Original) A modified human DNA sequence which will hybridize to a portion of target human DNA, said sequence comprising a single copy human DNA sequence of known sequence having a length of at least about 2000 nucleotides and being free of the repeat sequences identified

as SEQ ID Nos. 1-428, 447-479, and subsequences thereof, said subsequences containing at least 17 nucleotides, at least a portion of the human nucleic acid sequence being derived from an intron or an intergenic region wherein an intergenic region begins either upstream of the transcription initiation site or downstream of the polyadenylation site, said human DNA sequence being modified so that it is detectable, and said probe being complementary to a non-repetitive portion of the target.

12. (Original) A nucleic acid hybridization probe comprising a labeled, human nucleic acid sequence having a length of at least about 2000 nucleotides and being free of SEQ ID Nos. 1-428 and 447-479 and 17 mer subsequences thereof, said probe being complementary to and hybridizable with a nonrepetitive portion of target human DNA, said target human DNA comprising the known sequence of the human genome, at least a portion of the human nucleic acid sequence being derived either from an intron or an intergenic region wherein an intergenic region begins either upstream of the transcription initiation site or downstream of the polyadenylation site, and said probe being complementary to a non-repetitive portion of the target.